How Bayesian inference can help winegrowers?

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Résumé. Les vignerons sont engagés à contrer les parasites qui menacent leurs vignobles. Les traitements phytosanitaires doivent être planifiés avec précision pour améliorer la qualité des produits, limiter les coûts, réduire l'impact environnemental, conformément aux directives européennes qui encouragent une utilisation durable des produits phytosanitaires. Le principal parasite dans les vignobles européens est l'Eudémis (*Lobesia botrana*) qui endommage les grappes quand il est au stade larvaire. Par conséquent, les vignerons sont intéressés à connaître la dynamique du parasite pour planifier les traitements phytosanitaires. Un modèle de dynamique de population basée sur équations aux dérivées partielles a été proposé pour décrire la variation de l'abondance des parasites en fonction du temps et de l'âge physiologique. Le modèle de population est basée sur les fonctions biodémographiques (développement, fécondité et survie), décrivant les réponses des parasites aux conditions environnementales. La plupart des données relatives à l'estimation des fonctions biodémographiques sont disponibles dans la littérature. Malheureusement, aucune donnée n'est disponible pour la mortalité extrinsèque. Nous proposons une approche bayésienne pour estimer cette mortalité à partir des données sur l'abondance de la population. Les estimations sont fournies en fonction de leur distribution a posteriori, en exploitant une méthode MCMC qui utilise le software STAN. La moyenne de toutes les dynamiques, obtenue avec 50 différentes valeurs pour chaque paramètre estimé, donne une bonne approximation de l'abondance de l'Eudémis dans le temps. Cela rend le modèle utile pour les vignerons pour soutenir la prise de décision pour la lutte antiparasitaire.

Mots-clés. Inférence bayésienne, algorithmes MCMC, dynamique des populations, parasites.

Abstract. Winegrowers are committed to tackle the pests threatening their vineyards. Phytosanitary treatments have to be accurately planned to increase product quality, limit costs, and reduce environmental impact in compliance with the European guidelines that encourage a sustainable use of phytosanitary products. The main pest in European vineyards is the grape berry moth *Lobesia botrana* damaging grape bunches when it is in the larval stage. Consequently, winegrowers are interested in knowing the dynamics of this pest to carefully plan phytosanitary treatments. A population dynamics model based on partial differential equations has been proposed to describe the variation of the pest abundance in time and physiological age. The population model is based on biodemographic

functions (development, fecundity and survival rate functions), describing the individual life history responses to environmental conditions. Most of the data for the estimation of the stage-specific rate functions are available in literature. Unfortunately, no data are available for the extrinsic mortality. We propose a Bayesian approach to estimate this mortality starting from population abundance data collected in the field. Estimates are provided in terms of their posterior distribution, exploiting a MCMC method using STAN software. The mean of all the dynamics, obtained running the population dynamics model for 50 different values of each estimated parameter, give a good approximation of the grape berry moth abundance in time. This makes the model a suitable tool for winegrowers to support decision making for pest control.

Keywords. Bayesian inference, MCMC algorithms, population dynamics, pest.

1 Introduction

The sustainable use of phytosanitary products is one of the main target of the European Directive 2009/128/EC, in order to hinder the pests reducing environmental impact and increasing products quality. The main pest in European vineyards is the grape berry moth *Lobesia botrana* (CABI, 2014). This pest damages grape bunches when it is in the larval stage, mainly in the second and third generation. To draft a suitable plan of phytosanitary treatments it is important that the winegrowers are able to predict the dynamics of this pest. To this end, a population dynamics model based on a system of Fokker-Planck partial differential equations has been proposed in Gilioli et al. (2016) to describe the variation of the pest abundance in the different biological stages.The grape berry moth has been considered as a stage structured population, with three immature stages and a reproductive stage (adult). The life history of the individuals of the population is characterized by the temperature-dependent biodemographic functions: development, fecundity and mortality rate functions for each stage. These functions can be estimated using literature data, except for a term due to biotic factors that appears in the mortality rate function of each stage. We assume that these terms (one for each mortality rate function) do not depend on temperature and we consider them as random variables. We propose a Bayesian approach to estimate the posterior distributions of these terms starting from population abundance data collected in the field. Bayesian methods to estimate parameters in population dynamics have been already applied in recent years (Gillespie and Golightly, 2010; Gilioli et al., 2008 and 2012; Heydari, 2014; Martín-Fernández et al., 2014). The main advantage of obtaining posterior distributions is to have also an indication of the uncertainty associated to the estimates. The estimation procedure here presented is based on a MCMC method implemented in STAN software. For the case of the grape berry moth here analyzed, abundance data for all the stages, collected in three different years in the same location, are available. Two types of estimations have been performed for each parameter: estimation of a single posterior distribution obtained using

observation data of three different years in sequence, and estimation of three posterior distributions using the observations of each year individually. Population dynamics have been then obtained running the population dynamics model for 50 different values of each estimated parameter of the mortality functions, drawn from the corresponding posterior distributions. The mean of all the dynamics obtained give a good approximation of the grape berry moth abundance in time. The knowledge of the approximated abundance of each stage of the population makes the model a suitable tool for winegrowers to support decision making for threshold-based pest control.

2   Bayesian estimation for the mortality

The grape berry moth is considered as a stage-structured population with four stages: eggs, larvae, pupae and adults. The population dynamics is described through a system of Fokker-Planck partial differential equations (PDE) involving the stage-specific biodemographic functions of the species (development, mortality and fecundity rate functions) (Buffoni and Pasquali, 2007; Gilioli et al., 2016). The mortality function for each stage is composed by two terms: a function of the temperature, representing the intrinsic mortality due to abiotic factors, and a term representing the extrinsic mortality due to biotic factors that does not depend on temperature, but depends on the generation. The boundary conditions regulate the flux of the insect from a stage to the next one and the production of eggs for the adult stage. The solution to the PDE system gives the abundance of the population in each stage that depends on time and physiological age of the insect.

Development, fecundity and intrinsic mortality rate functions can be estimated using literature data. No data are available for the extrinsic mortality rate terms. These terms depend on the stage and on the generation of the population, and may vary from year to year. Three years of abundance data collected in Colognola ai Colli (Italy) are available to obtain an estimate of these terms.

Here we propose a Bayesian method to estimate the extrinsic mortality under two different scenario: constant extrinsic mortality for all the years and extrinsic mortality different for all the years. In the first case, starting from a prior distribution for each extrinsic mortality term we obtain, after the first year of available data, a posterior distribution that will be used as prior distribution for the second year. After the third year of collected data we obtain a posterior distribution for each parameter summarizing all the information coming from three years of observations. In the second case, each year is considered individually. Then, we start from the same prior distribution each year and we obtain, for each parameter, three different posterior distributions.

Since no information on the extrinsic mortality rate is available, the prior distribution used for each parameter the first year is always a uniform distribution. From Gilioli et al. (2016) we deduce that these terms cannot exceed 0.25, then we choose uniform prior distributions on the interval $[0, 0.25]$. As in many practical cases, the posterior
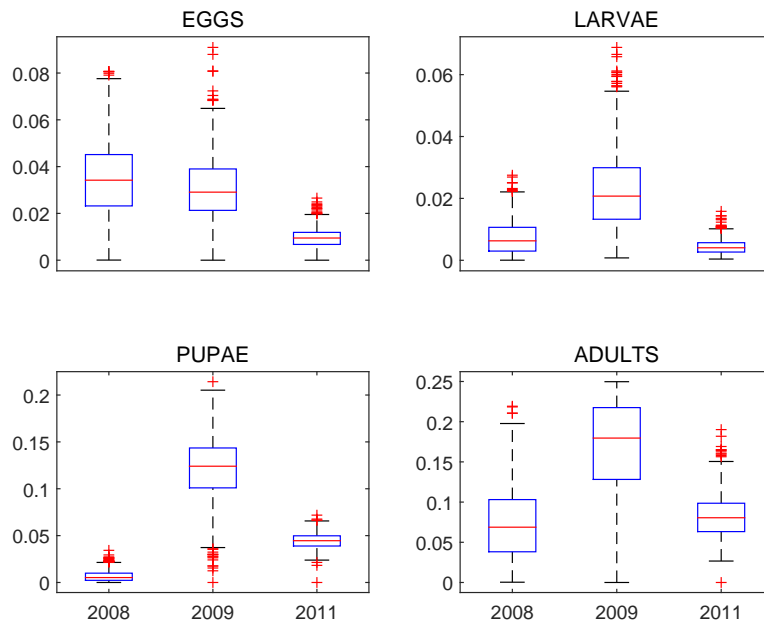
Figure 1: Box-plots of the posterior distributions of the extrinsic mortality term for the second generation of all the stages of the grape berry moth, for the years 2008, 2009, 2011.

distributions cannot be derived in a closed form; hence a MCMC method is used to approximate the posterior distributions. This is performed through STAN software that allows to obtain a quicker convergence and lower memory utilization with respect to other widely used tools (e.g., JAGS).

3   Results

Before applying the Bayesian estimated method to the field data case, we tested it on simulated data proving the convergence of the method. Moreover, we found that the posterior distributions of the extrinsic mortality terms can be well fitted with gamma distributions (truncated on the support of the uniform prior distributions).

In the case of field data, simulations do not show a trend for all the posterior distributions in the three years considered (see Figure 1 for the posterior distributions of eggs, larvae, pupae, and adults of the grape berry moth in the second generation). Consequently, the extrinsic mortality rates cannot be considered constant. This suggests to perform the estimation for all the three years separately.

To evaluate the goodness of the obtained estimates, we compare the trajectories of the population dynamics. Firstly, in the case of parameters estimated considering the data of the three years in sequence, we simulate the mean dynamics drawing 50 values
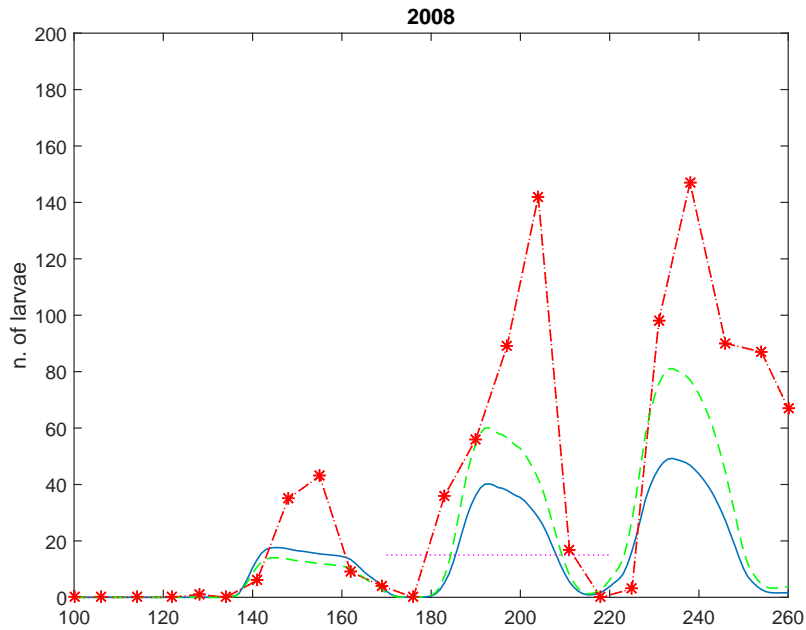
Figure 2: Sampled and simulated dynamics of the grape berry moth larvae for the year 2008. Asterisks represent field data in a vineyard in Colognola ai Colli (Italy), continuous line is the simulated dynamics obtained as mean of the trajectories for 50 values drawn from the final distribution of each parameter (considering the three years in sequence), dashed line is the simulated dynamics obtained as mean of the trajectories obtained drawing 50 values from the final distribution of each parameter (considering each year individually). Dotted line is the abundance control threshold for the second larval generation (15 larvae per 100 berry bunch, CABI 2014).

from the final distribution of each parameter (posterior distribution obtained after the third year). Then, we consider the data of each year individually obtaining different posterior distributions for each year. We use these posterior distributions to generate the mean dynamics, drawing 50 values from the final distribution of each parameter for each year. In the second case, mean square errors (calculated with respect to collected data) are smaller than in the case of the same posterior distribution for all the year for each parameter. This further confirms the time dependence of the extrinsic mortality rate terms.

Nevertheless, to the end of a control intervention based on abundance thresholds, we have not great differences in the two cases. In fact, considering that the most damaging stage is represented by the larvae of second generation, in both the cases the model correctly simulate the crossing of the abundance control threshold (Figure 2).

Then, the Bayesian estimation method here proposed, together with the population

dynamics model based on a system of Fokker-Planck differential equations, represents a useful tool to support decision making for pest control and allows to better plan the phytosanitary treatments increasing product quality and reducing environmental impact.

References

[1] Buffoni, G. and Pasquali, S. (2007), Structured population dynamics: continuous size and discontinuous stage structures, *Journal of Mathematical Biology*, 54(4), 555–595.

[2] CABI (2014), *Lobesia botrana* (grape berry moth), CABI Invasive Species Compendium, http://www.cabi.org/isc/datasheet/42794.

[3] Gilioli, G., Pasquali, S. and Marchesini, E. (2016), A modelling framework for pest population dynamics and management: an application to the grape berry moth, *Ecological Modelling*, 320, 348–357.

[4] Gilioli, G., Pasquali, S. and Ruggeri, F. (2008), Bayesian inference for functional response in a stochastic predator-prey system, *Bulletin of Mathematical Biology*, 70, 358–381.

[5] Gilioli, G., Pasquali, S. and Ruggeri, F. (2012), Nonlinear functional response parameter estimation in a stochastic predator-prey model, *Mathematical Biosciences and Engineering*, 9(1), 75–96.

[6] Gillespie, C.S. and Golightly, A. (2010), Bayesian inference for generalized stochastic population growth models with applications to aphids, *Journal of the Royal Statistical Society*, 59(2), 341–357.

[7] Martín-Fernández, L., Gilioli, G., Lanzarone, E., Míguez, J., Pasquali, S., Ruggeri, F. and Ruiz, D.P. (2014), A Rao-Blackwellized particle filter for joint parameter estimation and biomass tracking in a stochastic predator-prey system, *Mathematical Biosciences and Engineering*, 11(3), 573-597.